

SEQUENCE LISTING

- 5 SEQ ID NO: 1 is mouse TECK nucleotide sequence.
SEQ ID NO: 2 is mouse TECK amino acid sequence.
SEQ ID NO: 3 is human TECK nucleotide sequence.
SEQ ID NO: 4 is human TECK amino acid sequence.
SEQ ID NO: 5 is human MIP-3 α nucleotide sequence.
SEQ ID NO: 6 is human MIP-3 α amino acid sequence.
10 SEQ ID NO: 7 is human MIP-3 β nucleotide sequence.
SEQ ID NO: 8 is human MIP-3 β amino acid sequence.
SEQ ID NO: 9 is human DC CR nucleotide sequence.
SEQ ID NO: 10 is human DC CR amino acid sequence.
SEQ ID NO: 11 is human M/DC CR nucleotide sequence.
15 SEQ ID NO: 12 is human M/DC CR amino acid sequence.
SEQ ID NO: 13 is human CCKR1 amino acid sequence.
SEQ ID NO: 14 is human CCKR2 amino acid sequence.
SEQ ID NO: 15 is human CCKR3 amino acid sequence.
SEQ ID NO: 16 is human CCKR4 amino acid sequence.
20 SEQ ID NO: 17 is HPRT sense primer.
SEQ ID NO: 18 is HPRT antisense primer.
SEQ ID NO: 19 is FLAG epitope tag sequence.
- 25 (1) GENERAL INFORMATION:
- (i) APPLICANT: Wang, Wei
Gish, Kurt C.
Schall, Thomas J.
30 Vicari, Alain P.
Zlotnik, Albert
- (ii) TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
- 35 (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
40 (C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104
- 45 (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
50
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
55
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/675,814
(B) FILING DATE: 05-JUL-1996
60 provisional filings DX0589P, DX0589P1; DX0589P2

various

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: DX0589Q1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415-852-9196
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 94..525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

30 AGGCTACAAG CAGGCACCAG CTCTCAGGAC CAGAAAGGCA TTGGTGGCCC CCTTAAACCT 60
TCAGGTATCT GGAGAGGAGA TCTAACCTTC ACT ATG AAA CTG TGG CTT TTT GCC 114
Met Lys Leu Trp Leu Phe Ala
1 5
35 TGC CTG GTT GCC TGT TTT GTT GGG GCC TGG ATG CCG GTT GTC CAT GCC 162
Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala
10 15 20
40 CAA GGT GCC TTT GAA GAC TGC TGC CTG GGT TAC CAG CAC AGG ATC AAA 210
Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys
25 30 35
45 TGG AAT GTT CTC CGG CAT GCT AGG AAT TAT CAC CAG CAG GAA GTG AGT 258
Trp Asn Val Leu Arg His Ala Arg Asn Tyr His Gln Gln Glu Val Ser
40 45 50 55
50 GGA AGC TGC AAC CTA CGT GCT GTG AGA TTC TAC TTC CGC CAG AAA GTA 306
Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val
60 65 70
GTG TGT GGG AAT CCA GAG GAC ATG AAT GTG AAG AGG GCG ATA AGA ATC 354
Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile
75 80 85
55 TTG ACA GCT AGG AAA AGG CTA GTC CAC TGG AAG AGC GCG TCA GAC TCT 402
Leu Thr Ala Arg Lys Arg Leu Val His Trp Lys Ser Ala Ser Asp Ser
90 95 100
60 CAG ACT GAA AGG AAG AAG TCA AAC CAT ATG AAG TCC AAG GTG GAG AAC 450

Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn
 105 110 115
 5 CCC AAC AGT ACA AGC GTG AGG AGT GCC ACC CTA GGT CAT CCC AGG ATG 498
 Pro Asn Ser Thr Ser Val Arg Ser Ala Thr Leu Gly His Pro Arg Met
 120 125 130 135
 GTG ATG ATG CCC AGA AAG ACC AAC AAT TAAGTTAATT ACTCAGAGTA 545
 Val Met Met Pro Arg Lys Thr Asn Asn
 10 140
 AGCACCAGCT GGAGGATGGG CGGAGTCTGC TGAAGTGCTG TCTTCTAGGC ATGCCAGTGC 605
 CAATGAACTC ACTGAAGCTA CAGTTTCCTG TACAAGACCA GACCCACCAA CGTCTCAGCA 665
 15 TGTACGAGGA AGGAACTACT GCGCTAAAGG CCCTCCCACT CACCAAGGAG CTATTGGCTA 725
 TTGATGATTG CTGAGGGAAG GGAGTAATTT TTTTCTCTT TCTGAAGTGT GACTTGAGTA 785
 20 AATTGCCCCAT AGTTCAGTAT ATAATCCCCA ACCTGTGCTC AGGCAAGCAA CCCTAATTAA 845
 ATGCAATAGC CACATACAAA AGAAGAGGAT ATGAATAGTT TGGTAGGAGG GGCTTGTTAG 905
 GAAGAAGACA TTAACAGGAG AGAGAGGAGC GAGAGGATAG TGAGTGTGTG AGAGTGCCTG 965
 25 CACGTGTGAA ATGGTCAAAG AATTAAAAA TAAAACTTA AAAAGCTATT AAAAAGTAAA 1025
 AAAAAATAAA 1034

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu Trp Leu Phe Ala Cys Leu Val Ala Cys Phe Val Gly Ala
 1 5 10 15
 45 Trp Met Pro Val Val His Ala Gln Gly Ala Phe Glu Asp Cys Cys Leu
 20 25 30
 Gly Tyr Gln His Arg Ile Lys Trp Asn Val Leu Arg His Ala Arg Asn
 35 40 45
 50 Tyr His Gln Gln Glu Val Ser Gly Ser Cys Asn Leu Arg Ala Val Arg
 50 55 60
 55 Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn
 65 70 75 80
 Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His
 85 90 95
 60 Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His

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100

105

110

Met Lys Ser Lys Val Glu Asn Pro Asn Ser Thr Ser Val Arg Ser Ala
115 120 125

Thr Leu Gly His Pro Arg Met Val Met Met Pro Arg Lys Thr Asn Asn
130 135 140

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1012 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 117..566

(ix) FEATURE:

(A) NAME/KEY: mat. peptide

(B) LOCATION: 186..566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACCCACG CGTCCGCTTG GCCTACAGCC CGGCGGGCAT CAGCTCCCTT GACCCAGTGG 60
ATATCGGTGG CCCCGTTATT CGTCCAGGTG CCCAGGGAGG AGGACCCGCC TGCAGC 116
ATG AAC CTG TGG CTC CTG GCC TGC CTG GTG GCC GGC TTC CTG GGA GCC 164
Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
-23 -20 -15 -10
TGG GCC CCC GCT GTC CAC ACC CAA GGT GTC TTT GAG GAC TGC TGC CTG 212
Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
-5 1 5
GCC TAC CAC TAC CCC ATT GGG TGG GCT GTG CTC CGG CGC GCC TGG ACT 260
Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
10 15 20 25
TAC CGG ATC CAG GAG GTG AGC GGG AGC TGC AAT CTG CCT GCT GCG ATA 308
Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
30 35 40
TTC TAC CTC CCC AAG AGA CAC AGG AAG GTG TGT GGG AAC CCC AAA AGC 356
Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
45 50 55
AGG GAG GTG CAG AGA GCC ATG AAG CTC CTG GAT GCT CGA AAT AAG GTT 404
Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
60 65 70
TTT GCA AAG CTC CAC CAC AAC ATG CAG ACC TTC CAA GCA GGC CCT CAT 452

Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His
75 80 85
5 GCT GTA AAG AAG TTG AGT TCT GGA AAC TCC AAG TTA TCA TCA TCC AAG 500
Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys
90 95 100 105
10 TTT AGC AAT CCC ATC AGC AGC AGC AAG AGG AAT GTC TCC CTC CTG ATA 548
Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile
110 115 120
15 TCA GCT AAT TCA GGA CTG TGAGCCGGCT CATTTCTGGG CTCCATCGGC 596
Ser Ala Asn Ser Gly Leu
125
ACAGGAGGGG CCGGATCTTT CTCCGATAAA ACCGTCGCCC TACAGACCCA GCTGTCCCCA 656
CGCCTCTGTC TTTTGGGTCA AGTCTTAATC CCTGCACCTG AGTTGGTCCT CCCTCTGCAC 716
20 CCCCACCACC TCCTGCCCCG CTGGCAACTG GAAAGAAGGA GTTGGCCTGA TTTTAACCTT 776
TTGCCGCTCC GGGGAACAGC ACAATCCTGG GCAGCCAGTG GCTCTTGTAG AGAAACTTA 836
25 GGATACCTCT CTCACCTTCT GTTTCTTGGC GTCCACCCCG GGCCATGCCA GTGTGTCTCTC 896
TGGGTCCCCT CCAAAAATCT GGTCATTCAA GGATCCCCTC CCAAGGCTAT GCTTTTCTAT 956
AACTTTTAAA TAAACCTTGG GGGGTGAATG GAATAAAAAA AAAAAAAAAA AAAAAA 1012

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
-23 -20 -15 -10
45 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
-5 1 5
Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
10 15 20 25
50 Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
30 35 40
Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
55 45 50 55
Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
60 65 70
60 Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His

75 80 85

Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys
90 95 100 105

5 Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile
110 115 120

10 Ser Ala Asn Ser Gly Leu
125

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..288

25 (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 79..288

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35 ATG TGC TGT ACC AAG AGT TTG CTC CTG GCT GCT TTG ATG TCA GTG CTG 48
 Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
 -26 -25 -20 -15

40 CTA CTC CAC CTC TGC GGC GAA TCA GAA GCA GCA AGC AAC TTT GAC TGC 96
 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
 -10 -5 1 5

45 TGT CTT GGA TAC ACA GAC CGT ATT CTT CAT CCT AAA TTT ATT GTG GGC 144
 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
 10 15 20

50 TTC ACA CGG CAG CTG GCC AAT GAA GGC TGT GAC ATC AAT GCT ATC ATC 192
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35

55 TTT CAC ACA AAG AAA AAG TTG TCT GTG TGC GCA AAT CCA AAA CAG ACT 240
 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
 40 45 50

60 TGG GTG AAA TAT ATT GTG CGT CTC CTC AGT AAA AAA GTC AAG AAC ATG 288
 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
 55 60 65 70

TAAAAACTGT GGCTTTTCTG GAATGGAATT GGACATAGCC CAAGAACAGA AAGAACCCTTG 348

60 CTGGGGTTGG AGGTTTCACT TGCACATCAT GGAGGGTTTA GTGCTTATCT AATTTGTGCC 408

5 TCACTGGACT TGTCCAATTA ATGAAGTTGA TTCATATTGC ATCATAGTTT GCTTTGTTTA 468
AGCATCACAT TAAAGTTAAA CTGTATTTTA TGTTATTTAT AGCTGTAGGT TTTCTGTGTT 528
TAGCTATTTA ATACTAATTT TCCATAAGCT ATTTTGTTTT AGTGCAAAGT ATAAAATTAT 588
ATTTGGGGGG GAATAAGATT ATATGGACTT TTTTGCAAGC AACAAGCTAT TTTTAAAAA 648
10 AAACATTTTA ACATTCTTTT GTTTATATTG TTTTGTCTCC TAAATTGTTG TAATTGCATT 708
ATAAAATAAG AAAAATATTA ATAAGACAAA TATTGAAAAT AAAGAAACAA AAAGTTAAAA 768
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 801

(2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

30 Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
-26 -25 -20 -15
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
-10 -5 1 5
35 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
10 15 20
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
25 30 35
40 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
40 45 50
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
55 60 65 70

(2) INFORMATION FOR SEQ ID NO:7:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 699 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

60 (A) NAME/KEY: CDS
(B) LOCATION: 142..435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5 GGCACGAGCG GCACGAGCAT CACTCACACC TTGCATTTCA CCCCTGCATC CCAGTCGCCC 60
 TGCAGCCTCA CACAGATCCT GCACACACCC AGACAGCTGG CGCTCACACA TTCACCGTTG 120
 GCCTGCCTCT GTTCACGCTC C ATG GCC CTG CTA CTG GCC CTC AGC CTG CTG 171
 10 Met Ala Leu Leu Leu Ala Leu Ser Leu Leu
 1 5 10
 GTT CTC TGG ACT TCC CCA GCC CCA ACT CTG AGT GGC ACC AAT GAT GCT 219
 Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala
 15 15 20 25
 GAA GAC TGC TGC CTG TCT GTG ACC CAG AAA CCC ATC CCT GGG TAC ATC 267
 Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile
 30 35 40
 20 GTG AGG AAC TTC CAC TAC CTT CTC ATC AAG GAT GGC TGC AGG GTG CCT 315
 Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg Val Pro
 45 50 55
 25 GCT GTA GTG TTC ACC ACA CTG AGG GGC CGC CAG CTC TGT GCA CCC CCA 363
 Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro
 60 65 70
 GAC CAG CCC TGG GTA GAA CGC ATC ATC CAG AGA CTG CAG AGG ACC TCA 411
 30 Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser
 75 80 85 90
 GCC AAG ATG AAG CGC CGC AGC AGT TAACCTATGA CCGTGCAGAG GGAGCCCCGA 465
 35 Ala Lys Met Lys Arg Arg Ser Ser
 95
 GTCCGAGTCA AGCATTGTGA ATTATTACCT AACCTGGGGA ACCGAGGACC AGAAGGAAGG 525
 ACCAGGCTTC CAGCTCCTCT GCACCAGACC TGACCAGCCA GGACAGGGCC TGGGGTGTGT 585
 40 GTGAGTGTGA GTGTGAGCGA GAGGGTGAGT GTGGTCTAGA GTAAAGCTGC TCCACCCCCA 645
 GATTGCAATG CTACCAATAA AGCCGCCTGG TGTTTACAAC TAAAAAAAAA AAAA 699

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
 1 5 10 15
 60 Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser

20 25 30

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
35 40 45

5 Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
50 55 60

10 Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
65 70 75 80

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Arg Arg
85 90 95

15 Ser Ser

(2) INFORMATION FOR SEQ ID NO:9:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

30 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1095

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

48
ATG TTT TCG ACT CCA GTG AAG ATT ATT TTG TGT CAG TCA ATA CTT CAT
Met Phe Ser Thr Pro Val Lys Ile Ile Leu Cys Gln Ser Ile Leu His
1 5 10 15

96
40 ATT ACT CAG TTG ATT CTG AGA TGT TAC TGT GCT CCT TGC AGG AGG TCA
Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser
20 25 30

144
45 GGC AGT TCT CCA GGC TAT TTG TAC CGA ATT GCC TAC TCC TTG ATC TGT
Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys
35 40 45

192
50 GTT CTT GGC CTC CTG GGG AAT ATT CTG GTG GTG ATC ACC TTT GCT TTT
Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe
50 55 60

240
TAT AAG AAG GCC AGG TCT ATG ACA GAC GTC TAT CTG TTG AAC ATG GCC
Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
65 70 75 80

288
55 ATT GCA GAC ATC CTC TTT GTT CTT ACT CTC CCA TTC TCG GCA GTG AGT
Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser
85 90 95

336
60 CAT GCC ACT GGT GCG TGG GTT TTC AGC AAT GCC ACG TGC AAG TTG CTA

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	His	Ala	Thr	Gly	Ala	Trp	Val	Phe	Ser	Asn	Ala	Thr	Cys	Lys	Leu	Leu	
				100					105					110			
5	AAA Lys	GGC Gly	ATC Ile	TAT Tyr	GCC Ala	ATC Ile	AAC Asn	TTT Phe	AAC Asn	TGC Cys	GGG Gly	ATG Met	CTG Leu	CTC Leu	CTG Leu	ACT Thr	384
10	TGC Cys	ATT Ile	AGC Ser	ATG Met	GAC Asp	CGG Arg	TAC Tyr	ATC Ile	GCC Ala	ATT Ile	GTA Val	CAG Gln	GCG Ala	ACT Thr	AAG Lys	TCA Ser	432
15	TTC Phe	CGG Arg	CTC Leu	CGA Arg	TCC Ser	AGA Arg	ACA Thr	CTA Leu	CCG Pro	CGC Arg	AGC Ser	AAA Lys	ATC Ile	ATC Ile	TGC Cys	CTT Leu	480
20	GTT Val	GTG Val	TGG Trp	GGG Gly	CTG Leu	TCA Ser	GTC Val	ATC Ile	ATC Ile	TCC Ser	AGC Ser	TCA Ser	ACT Thr	TTT Phe	GTC Val	TTC Phe	528
25	AAC Asn	CAA Gln	AAA Lys	TAC Tyr	AAC Asn	ACC Thr	CAA Gln	GGC Gly	AGC Ser	GAT Asp	GTC Val	TGT Cys	GAA Glu	CCC Pro	AAG Lys	TAC Tyr	576
30	CAA Gln	ACT Thr	GTC Val	TCG Ser	GAG Glu	CCC Pro	ATC Ile	AGG Arg	TGG Trp	AAG Lys	CTG Leu	CTG Leu	ATG Met	TTG Leu	GGG Gly	CTT Leu	624
35	GAG Glu	CTA Leu	CTC Leu	TTT Phe	GGT Gly	TTC Phe	TTT Phe	ATC Ile	CCT Pro	TTG Leu	ATG Met	TTC Phe	ATG Met	ATA Ile	TTT Phe	TGT Cys	672
40	TAC Tyr	ACG Thr	TTC Phe	ATT Ile	GTC Val	AAA Lys	ACC Thr	TTG Leu	GTG Val	CAA Gln	GCT Ala	CAG Gln	AAT Asn	TCT Ser	AAA Lys	AGG Arg	720
45	CAC His	AAA Lys	GCC Ala	ATC Ile	CGT Arg	GTA Val	ATC Ile	ATA Ile	GCT Ala	GTG Val	GTG Val	CTT Leu	GTG Val	TTT Phe	CTG Leu	GCT Ala	768
50	TGT Cys	CAG Gln	ATT Ile	CCT Pro	CAT His	AAC Asn	ATG Met	GTC Val	CTG Leu	CTT Leu	GTG Val	ACG Thr	GCT Ala	GCT Ala	AAT Asn	TTG Leu	816
55	GGT Gly	AAA Lys	ATG Met	AAC Asn	CGA Arg	TCC Ser	TGC Cys	CAG Gln	AGC Ser	GAA Glu	AAG Lys	CTA Leu	ATT Ile	GGC Gly	TAT Tyr	ACG Thr	864
60	AAA Lys	ACT Thr	GTC Val	ACA Thr	GAA Glu	GTC Val	CTG Leu	GCT Ala	TTC Phe	CTG Leu	CAC His	TGC Cys	TGC Cys	CTG Leu	AAC Asn	CCT Pro	912
65	GTG Val	CTC Leu	TAC Tyr	GCT Ala	TTT Phe	ATT Ile	GGG Gly	CAG Gln	AAG Lys	TTC Phe	AGA Arg	AAC Asn	TAC Tyr	TTT Phe	CTG Leu	AAG Lys	960
70	ATC Ile	TTG Leu	AAG Lys	GAC Asp	CTG Leu	TGG Trp	TGT Cys	GTG Val	AGA Arg	AGG Lys	AAG Lys	TAC Tyr	AAG Lys	TCC Ser	TCA Ser	GGC Gly	1008
75	TTC Phe	TCC Leu	TGT Trp	GCC Ala	GGG Gly	AGG Arg	TAC Thr	TCA Leu	GAA Pro	AAC Arg	ATT Lys	TCT Cys	CGG Gln	CAG Gln	ACC Gly	AGT Ser	1056

Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser
340 345 350

5 GAG ACC GCA GAT AAC GAC AAT GCG TCG TCC TTC ACT ATG TGATAGAAAG 1105
Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met
355 360 365

CTGAGTCTCC CTAA 1119

10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Ser Thr Pro Val Lys Ile Ile Leu Cys Gln Ser Ile Leu His
1 5 10 15

25 Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser
20 25 30

Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys
35 40 45

30 Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe
50 55 60

35 Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
65 70 75 80

Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser
85 90 95

40 His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu
100 105 110

Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr
115 120 125

45 Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
130 135 140

50 Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu
145 150 155 160

Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe
165 170 175

55 Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr
180 185 190

Gln Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu
195 200 205

60

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	Glu	Leu	Leu	Phe	Gly	Phe	Phe	Ile	Pro	Leu	Met	Phe	Met	Ile	Phe	Cys
	210							215						220		
5	Tyr	Thr	Phe	Ile	Val	Lys	Thr	Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg
	225					230					235					240
	His	Lys	Ala	Ile	Arg	Val	Ile	Ile	Ala	Val	Val	Leu	Val	Phe	Leu	Ala
					245					250					255	
10	Cys	Gln	Ile	Pro	His	Asn	Met	Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Leu
				260					265					270		
	Gly	Lys	Met	Asn	Arg	Ser	Cys	Gln	Ser	Glu	Lys	Leu	Ile	Gly	Tyr	Thr
			275					280					285			
15	Lys	Thr	Val	Thr	Glu	Val	Leu	Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro
		290					295					300				
20	Val	Leu	Tyr	Ala	Phe	Ile	Gly	Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Leu	Lys
	305					310					315					320
	Ile	Leu	Lys	Asp	Leu	Trp	Cys	Val	Arg	Arg	Lys	Tyr	Lys	Ser	Ser	Gly
				325						330					335	
25	Phe	Ser	Cys	Ala	Gly	Arg	Tyr	Ser	Glu	Asn	Ile	Ser	Arg	Gln	Thr	Ser
				340					345					350		
	Glu	Thr	Ala	Asp	Asn	Asp	Asn	Ala	Ser	Ser	Phe	Thr	Met			
			355					360					365			

(2) INFORMATION FOR SEO ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 49..1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

50	GAGGAAGCTG	CTTCGGGGGG	TGAGCAAACT	TTTTAAATG	CAGAAATT	ATG	ATC	TAC	57								
						Met	Ile	Tyr									
						1											
55	ACC	CGT	TTC	TTA	AAA	GGC	AGT	CTG	AAG	ATG	GCC	AAT	TAC	ACG	CTG	GCA	105
	Thr	Arg	Phe	Leu	Lys	Gly	Ser	Leu	Lys	Met	Ala	Asn	Tyr	Thr	Leu	Ala	
	5						10					15					
60	CCA	GAG	GAT	GAA	TAT	GAT	GTC	CTC	ATA	GAA	GGT	GAA	CTG	GAG	AGC	GAT	153
	Pro	Glu	Asp	Glu	Tyr	Asp	Val	Leu	Ile	Glu	Gly	Glu	Leu	Glu	Ser	Asp	
	20					25					30				35		

	GAG	GCA	GAG	CAA	TGT	GAC	AAG	TAT	GAC	GCC	CAG	GCA	CTC	TCA	GCC	CAG	201
	Glu	Ala	Glu	Gln	Cys	Asp	Lys	Tyr	Asp	Ala	Gln	Ala	Leu	Ser	Ala	Gln	
				40						45					50		
5	CTG	GTG	CCA	TCA	CTC	TGC	TCT	GCT	GTG	TTT	GTG	ATC	GGT	GTC	CTG	GAC	249
	Leu	Val	Pro	Ser	Leu	Cys	Ser	Ala	Val	Phe	Val	Ile	Gly	Val	Leu	Asp	
			55						60					65			
10	AAT	CTC	CTG	GTT	GTG	CTT	ATC	CTG	GTA	AAA	TAT	AAA	GGA	CTC	AAA	CGC	297
	Asn	Leu	Leu	Val	Val	Leu	Ile	Leu	Val	Lys	Tyr	Lys	Gly	Leu	Lys	Arg	
			70					75					80				
15	GTG	GAA	AAT	ATC	TAT	CTT	CTA	AAC	TTG	GCA	GTT	TCT	AAC	TTG	TGT	TTC	345
	Val	Glu	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Val	Ser	Asn	Leu	Cys	Phe	
		85					90					95					
20	TTG	CTT	ACC	CTG	CCC	TTC	TGG	GCT	CAT	GCT	GGG	GGC	GAT	CCC	ATG	TGT	393
	Leu	Leu	Thr	Leu	Pro	Phe	Trp	Ala	His	Ala	Gly	Gly	Asp	Pro	Met	Cys	
	100					105					110					115	
25	AAA	ATT	CTC	ATT	GGA	CTG	TAC	TTC	GTG	GGC	CTG	TAC	AGT	GAG	ACA	TTT	441
	Lys	Ile	Leu	Ile	Gly	Leu	Tyr	Phe	Val	Gly	Leu	Tyr	Ser	Glu	Thr	Phe	
					120					125					130		
30	TTC	AAT	TGC	CTT	CTG	ACT	GTG	CAA	AGG	TAC	CTA	GTG	TTT	TTG	CAC	AAG	489
	Phe	Asn	Cys	Leu	Leu	Thr	Val	Gln	Arg	Tyr	Leu	Val	Phe	Leu	His	Lys	
				135				140						145			
35	GGC	AAC	TTT	TTC	TCA	GCC	AGG	AGG	AGG	GTG	CCC	TGT	GGC	ATC	ATT	ACA	537
	Gly	Asn	Phe	Phe	Ser	Ala	Arg	Arg	Arg	Val	Pro	Cys	Gly	Ile	Ile	Thr	
			150				155						160				
40	AGT	GTC	CTG	GCA	TGG	GTA	ACA	GCC	ATT	CTG	GCC	ACT	TTG	CCT	GAA	TTC	585
	Ser	Val	Leu	Ala	Trp	Val	Thr	Ala	Ile	Leu	Ala	Thr	Leu	Pro	Glu	Phe	
		165					170					175					
45	GTG	GTT	TAT	AAA	CCT	CAG	ATG	GAA	GAC	CAG	AAA	TAC	AAG	TGT	GCA	TTT	633
	Val	Val	Tyr	Lys	Pro	Gln	Met	Glu	Asp	Gln	Lys	Tyr	Lys	Cys	Ala	Phe	
	180					185					190					195	
50	AGC	AGA	ACT	CCC	TTC	CTG	CCA	GCT	GAT	GAG	ACA	TTC	TGG	AAG	CAT	TTT	681
	Ser	Arg	Thr	Pro	Phe	Leu	Pro	Ala	Asp	Glu	Thr	Phe	Trp	Lys	His	Phe	
					200					205					210		
55	CTG	ACT	TTA	AAA	ATG	AAC	ATT	TCG	GTT	CTT	GTC	CTC	CCC	CTA	TTT	ATT	729
	Leu	Thr	Leu	Lys	Met	Asn	Ile	Ser	Val	Leu	Val	Leu	Pro	Leu	Phe	Ile	
				215					220					225			
60	TTT	ACA	TTT	CTC	TAT	GTG	CAA	ATG	AGA	AAA	ACA	CTA	AGG	TTC	AGG	GAG	777
	Phe	Thr	Phe	Leu	Tyr	Val	Gln	Met	Arg	Lys	Thr	Leu	Arg	Phe	Arg	Glu	
			230					235					240				
65	CAG	AGG	TAT	AGC	CTT	TTC	AAG	CTT	GTT	TTT	GCC	GTA	ATG	GTA	GTC	TTC	825
	Gln	Arg	Tyr	Ser	Leu	Phe	Lys	Leu	Val	Phe	Ala	Val	Met	Val	Val	Phe	
		245					250					255					
70	CTT	CTG	ATG	TGG	GCG	CCC	TAC	AAT	ATT	GCA	TTT	TTC	CTG	TCC	ACT	TTC	873
	Leu	Leu	Met	Trp	Ala	Pro	Tyr	Asn	Ile	Ala	Phe	Phe	Leu	Ser	Thr	Phe	
	260					265					270					275	

	AAA GAA CAC TTC TCC CTG AGT GAC TGC AAG AGC AGC TAC AAT CTG GAC	921
	Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr Asn Leu Asp	
	280 285 290	
5	AAA AGT GTT CAC ATC ACT AAA CTC ATC GCC ACC ACC CAC TGC TGC ATC	969
	Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His Cys Cys Ile	
	295 300 305	
10	AAC CCT CTC CTG TAT GCG TTT CTT GAT GGG ACA TTT AGC AAA TAC CTC	1017
	Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu	
	310 315 320	
15	TGC CGC TGT TTC CAT CTG CGT AGT AAC ACC CCA CTT CAA CCC AGG GGG	1065
	Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly	
	325 330 335	
20	CAG TCT GCA CAA GGC ACA TCG AGG GAA GAA CCT GAC CAT TCC ACC GAA	1113
	Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu	
	340 345 350 355	
	GTG TAAACTAGCA TCCACCAAAT GCAAGAAGAA TAAACATGGA TTTTCATCTT	1166
	Val	
25	TCTGCATTAT TTCATGTAAA TTTTCTAC ATTTGTATAC AAAATCGGAT ACAGGAAGAA	1226
	AAGGGAGAGG TGAGCTAACA TTTGCTAAC ACTGAATTG TCTCAGGCAC CGTGCAAGGC	1286
30	TCTTTACAAA CGTGAGCTCC TTCGCCTCCT ACCACTTGTC CATAGTGTGG ATAGGACTAG	1346
	TCTCATTTCT CTGAGAAGAA AACTAAGGCG CGGAAATTG TCTAAGATCA CATAACTAGG	1406
	AAGTGGCAGA ACTGATTCTC CAGCCCTGGT AGCATTGCT CAGAGCCTAC GCTTGGTCCA	1466
35	GAACATCAAA CTCCAAACCC TGGGGACAAA CGACATGAAA TAAATGTATT TTAAACATA	1526
	TAAAAAAAAA AAAAAAAAAA A	1547
40	(2) INFORMATION FOR SEQ ID NO:12:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 356 amino acids	
	(B) TYPE: amino acid	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
50	Met Ile Tyr Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr	
	1 5 10 15	
55	Thr Leu Ala Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu	
	20 25 30	
	Glu Ser Asp Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu	
	35 40 45	
60	Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly	

50 55 60

Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly
65 70 75 80

5 Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn
85 90 95

10 Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp
100 105 110

Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser
115 120 125

15 Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe
130 135 140

Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly
145 150 155 160

20 Ile Ile Thr Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu
165 170 175

25 Pro Glu Phe Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys
180 185 190

Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp
195 200 205

30 Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro
210 215 220

Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg
225 230 235 240

35 Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met
245 250 255

Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu
260 265 270

40 Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr
275 280 285

45 Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His
290 295 300

Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser
305 310 315 320

50 Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln
325 330 335

Pro Arg Gly Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His
340 345 350

55 Ser Thr Glu Val
355

60 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
1 5 10 15
Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
20 25 30
Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
35 40 45
Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
50 55 60
Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80
Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
85 90 95
Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
100 105 110
Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
115 120 125
Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
130 135 140
Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu
145 150 155 160
Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
165 170 175
Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
180 185 190
Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
195 200 205
Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
210 215 220
Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
225 230 235 240
Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn

(2) INFORMATION FOR SEQ ID NO:14:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40	Met	Leu	Ser	Thr	Ser	Arg	Ser	Arg	Phe	Ile	Arg	Asn	Thr	Asn	Glu	Ser
	1				5					10					15	
	Gly	Glu	Glu	Val	Thr	Thr	Phe	Phe	Asp	Tyr	Asp	Tyr	Gly	Ala	Pro	Cys
				20					25					30		
45	His	Lys	Phe	Asp	Val	Lys	Gln	Ile	Gly	Ala	Gln	Leu	Leu	Pro	Pro	Leu
			35					40					45			
	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	Met	Leu	Val	Val
		50					55					60				
50	Leu	Ile	Leu	Ile	Asn	Cys	Lys	Lys	Leu	Lys	Cys	Leu	Thr	Asp	Ile	Tyr
	65					70					75					80
	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Leu	Ile	Thr	Leu	Pro
55					85					90					95	
	Leu	Trp	Ala	His	Ser	Ala	Ala	Asn	Glu	Trp	Val	Phe	Gly	Asn	Ala	Met
				100					105					110		
60	Cys	Lys	Leu	Phe	Thr	Gly	Leu	Tyr	His	Ile	Gly	Tyr	Phe	Gly	Gly	Ile

115 120 125
 Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
 130 135 140
 5 Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
 145 150 155 160
 10 Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
 165 170 175
 Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 180 185 190
 15 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 195 200 205
 20 Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 210 215 220
 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 225 230 235 240
 25 Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 245 250 255
 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270
 30 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
 275 280 285
 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300
 35 Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
 305 310 315 320
 40 Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
 325 330 335
 Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
 340 345 350
 45 Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
 355 360 365
 Gln Asp Lys Glu Gly Ala
 370

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Residue Number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60										
Met	Thr	Thr	Ser	Leu	Asp	Thr	Val	Glu	Thr	Phe	Gly	Thr	Thr	Ser	Tyr																																																							
1				5					10					15																																																								
Tyr	Asp	Asp	Val	Gly	Leu	Leu	Cys	Glu	Lys	Ala	Asp	Thr	Arg	Ala	Leu																																																							
			20					25					30																																																									
Met	Ala	Gln	Phe	Val	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Thr	Val	Gly																																																							
		35					40					45																																																										
Leu	Leu	Gly	Asn	Val	Val	Val	Val	Met	Ile	Leu	Ile	Lys	Tyr	Arg	Arg																																																							
		50				55					60																																																											
Leu	Arg	Ile	Met	Thr	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp																																																							
65					70					75				80																																																								
Leu	Leu	Phe	Leu	Val	Thr	Leu	Pro	Phe	Trp	Ile	His	Tyr	Val	Arg	Gly																																																							
				85																																																																		

290 295 300
5 Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
305 310 315 320
Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
325 330 335
10 Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
340 345 350
Ile Val Phe
355

15 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 360 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

30 Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
1 5 10 15
Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
20 25 30
35 Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
35 40 45
40 Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
50 55 60
Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
65 70 75 80
45 Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
85 90 95
Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
100 105 110
50 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
115 120 125
Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
130 135 140
55 Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
145 150 155 160
60 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser

165 170 175

Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
180 185 190

5 Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
195 200 205

10 Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
210 215 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
225 230 235 240

15 Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
245 250 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
260 265 270

20 Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
275 280 285

25 Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
290 295 300

Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
305 310 315 320

30 Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
325 330 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
340 345 350

35 Asp His Asp Leu His Asp Ala Leu
355 360

(2) INFORMATION FOR SEQ ID NO:17:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

55 GTAATGATCA GTCAACGGGG GAC

23

(2) INFORMATION FOR SEQ ID NO:18:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGCAAGCT TGCAACCTTA ACCA

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Tyr Lys Asp Asp Asp Asp Lys Leu
1 5

1. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx = - \int_{\mathbb{R}^n} |\nabla u|^2 dx \leq 0$
 2. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx = - \int_{\mathbb{R}^n} |\nabla u|^2 dx \leq 0$
 3. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx = - \int_{\mathbb{R}^n} |\nabla u|^2 dx \leq 0$
 4. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx = - \int_{\mathbb{R}^n} |\nabla u|^2 dx \leq 0$
 5. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx = - \int_{\mathbb{R}^n} |\nabla u|^2 dx \leq 0$
 6. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx = - \int_{\mathbb{R}^n} |\nabla u|^2 dx \leq 0$
 7. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx = - \int_{\mathbb{R}^n} |\nabla u|^2 dx \leq 0$
 8. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx = - \int_{\mathbb{R}^n} |\nabla u|^2 dx \leq 0$
 9. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx = - \int_{\mathbb{R}^n} |\nabla u|^2 dx \leq 0$
 10. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx = - \int_{\mathbb{R}^n} |\nabla u|^2 dx \leq 0$